cells, washed, and then the percent binding measured by the ability of the samples to compete with Shh-Ig for binding to the cells. Bound Shh-Ig was quantified by mean fluorescence using a FITC-labeled anti-Ig antibody probe as the readout. The data were fitted to a hyberbolic curve by non-linear regression.

A marked-up version of the amended paragraphs is provided below.

Fig. 7. Analysis of Shh in a receptor binding assay. The relative potency of soluble (6) and tethered (~~8~~7) Shh for binding to *patched* was assessed on *patched*-transfected EBNA-293 cells by FACS analysis. Serial dilutions of the test samples were incubated with the EBNA-293 cells, washed, and then the percent binding measured by the ability of the samples to compete with Shh-Ig for binding to the cells. Bound Shh-Ig was quantified by mean fluorescence using a FITC-labeled anti-Ig antibody probe as the readout. The data were fitted to a hyberbolic curve by non-linear regression.

In the claims:

For the convenience of the Examiner, all claims being examined, whether or not amended, are presented below.

Please cancel, without prejudice, claim 62.

1. (**Twice Amended**) An isolated protein comprising an N-terminal amino acid and a C-terminal amino acid, wherein the protein comprises an amino acid sequence selected from:

(a) an amino acid sequence with an N-terminal cysteine that is appended with at least one hydrophobic moiety;

(b) an amino acid sequence with an N-terminal amino acid that is not a cysteine appended with at least one hydrophobic moiety; and